

```

QY 7634 taggcttaaacctggaactacaaagccaaagtcctccctgctgagggcagtaacctc 7693
Db 1 TAGGCTTAACCTGAGATCTACAAAGCCAAAGTCCCTCCCTGCTGAGGCGAGTACCTC 60
QY 7694 cattgggacagtcacagaccacagtcacaaagatgcccacattccttgccctcagccctcag 7753
Db 61 CATTTGGGACAGTCCAGACACCAAGTCAAGATGCCCATTCCTTGGGCTCAGCCCTCAG 120
QY 7754 ttcttcatttcacacagccgctgctgttgagttttcctccacagtgag 7805
Db 121 TTCTTCATTTCCACAGGCCGTGCTTGTGTGAGTTTCTCCACAGTGAG 172

RESULT 11
G15289/c
LOCUS       G15289             250 bp      DNA
DEFINITION  human STS SHCC-15950.
ACCESSION   G15289
VERSION     G15289.1  GI:1132052
KEYWORDS    STS sequence; primer; sequence tagged site.
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
Eukaryota; Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 250)
AUTHORS    Myers R.M.
JOURNAL    Unpublished (1995)
COMMENT    Contact: Richard M. Myers
            Stanford Human Genome Center (SHGC)
            Department of Medicine
            Department of Genetics, M-344, Stanford, CA 94305, USA
            Tel: 4157259687
            Fax: 4157259689
            Email: myers@shgc.stanford.edu

Primer A: TGCCACAAATAGTTTACATGGC
Primer B: GGACGGACCAAGCATCTGG
STS size: 131
PCR Profile:
  Initial incubation: 94 degrees C for 90 seconds
  Denaturation:      94 degrees C for 15 seconds
  Annealing:         62 degrees C for 23 seconds
  Polymerization:    72 degrees C for 30 seconds
  PCR Cycles:        30
  Thermal Cycler:    Perkin Elmer 9600
Protocol:
  Template:          25 ng
  Primer:             each 1 uM
  dNTPs:              each 200 uM
  Taq Polymerase:    0.05 units/ul
  Total Vol:         10 ul

Buffer:
  MgCl2:              2.5 mM
  KCl:                 50 mM
  Tris-HCl:           20 mM
  pH:                 8.3

Prepared with primer pairs derived from T65388--Merck/UniEST.
FEATURES             source
  source              1..250
                    /Location/Qualifiers
  STS                  /Organism="Homo sapiens"
  primer_bind          67..197
  primer_bind          67..88
  BASE_COUNT          85 a 48 c 43 g 65 t 9 others
  ORIGIN

```

```

Query Match
Best Local Similarity 1.1%; Score 98; DB 13; Length 250;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8947 agcttcattttttttgacgtcacctttttggccatgtaaacctatttggcaatttat 9006
Db 119 AGCTTCATTTATTTTTCAGCTCACCTTTTGGCCATTAACACTATTTGTGCAATTTAT 60
QY 9007 gtttttattatgaataaagaatgccatttctcagcc 9044
Db 59 GTTTTATTATGAATAAAGAATGCCATTTCTCAGGCC 22

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RESULT 12
AC012422/c
LOCUS       AC012422             53967 bp      DNA
DEFINITION  Homo sapiens chromosome 15 clone 141_E_4 map 15, LOW-PASS SEQUENCE
ACCESSION   AC012422
VERSION     AC012422.1  GI:6136396
KEYWORDS    HTG; HTGS_PHASE0.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 53967)
AUTHORS    Birren, B., Linton, L., Nusbaum, C. and Lander, E.
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 53967)
AUTHORS    Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
            Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Bouckhagter, B.,
            Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
            Cooke, P., DeArrellano, K., Devar, K., Domino, M., Donelan, L., Doyle, M.,
            Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D.,
            Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
            Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
            Lehoczy, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,
            McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J.,
            Morrison, K., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
            Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
            Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
            Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
            Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
            Submitted (27-OCT-1999) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
            All repeats were identified using RepeatMasker: Smit, A.F.A. &
            Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html.

```

* NOTE: This record contains 70 individual
 * sequencing reads that have not been assembled into
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 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.

```

1 722: contig of 722 bp in length
723 gap of unknown length
1504: contig of 782 bp in length
1505 gap of unknown length
2265: contig of 761 bp in length
2266 gap of unknown length
3025: contig of 760 bp in length
3026 gap of unknown length
3791: contig of 786 bp in length
3792 gap of unknown length
4608: contig of 817 bp in length
gap of unknown length

```

5 PAGE BLANK (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

IN nucleic - nucleic search, using sw model

Run on: April 19, 2000, 22:46:09 ; Search time 4891.93 Seconds

(Without alignments)
-5616.025 Million cell updates/sec

Title: PCT-US00-04950-1

Effect score: 9048

Sequence: 1 gcccctccagaagccctgcctc.....tgccattctcagccctct 9048

Coring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

searched: 821193 seqs, -1518192014 residues

ord size : 0

total number of hits satisfying chosen parameters: 1642386

inlunum DB seq length: 0

axlunum DB seq length: 1000000

ost-processing: Listing first 45 summaries

database :

GenFmb1.*
1: gb_bal.*
2: gb_ba2.*
3: gb_om.*
4: gb_ov.*
5: gb_pat.*
6: gb_ph.*
7: gb_pl1.*
8: gb_pl2.*
9: gb_pl3.*
10: gb_pr1.*
11: gb_pr2.*
12: gb_pr3.*
13: gb_ro.*
14: gb_sy.*
15: gb_un.*
16: gb_v1.*
17: em_fun.*
18: em_hum1.*
19: em_hum2.*
20: em_in.*
21: em_om.*
22: em_or.*
23: em_ov.*
24: em_pat.*
25: em_ph.*
26: em_pl.*
27: em_ro.*
28: em_sy.*
29: em_un.*
30: em_v1.*
31: em_v2.*
32: gb_hlg1.*
33: gb_hlg2.*
34: gb_hlg3.*
35: gb_hlg4.*
36: gb_hlg5.*
37: em_ba2.*
38: em_ba3.*
39: em_hum4.*
40: gb_pr4.*
41: gb_hlg3.*
42: gb_hlg4.*
43: gb_hlg5.*

44: gb_hlg6.*
45: gb_hlg7.*
46: em_hlg1.*
47: em_hlg2.*
48: em_hlg3.*
49: em_hum5.*
50: gb_pl3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9048	100.0	9108	40	AF123653 Homo sapi
2	4097	45.3	5492	40	AF123659 Homo sapi
3	757	8.4	1515	40	AF123656 Homo sapi
4	757	8.4	1614	40	AF123655 Homo sapi
5	757	8.4	1692	40	AF123657 Homo sapi
6	757	8.4	1722	40	AF123658 Homo sapi
7	346	3.8	633	40	AF123654 Homo sapi
8	172	1.9	172	13	G60003 Homo sapi
9	162	1.8	231	40	AF123652 Homo sapi
10	121	1.3	172	13	G43056 Homo sapi
11	98	1.1	250	13	G15289 Homo sapi
12	57	0.6	53967	42	AC012422 Homo sapi
13	57	0.6	165836	42	AC011963 Homo sapi
14	57	0.6	185893	11	AC005191 Homo sapi
15	55	0.6	197541	41	AC011371 Homo sapi
16	54	0.6	177596	33	HS88517 Homo sapi
17	53	0.6	37918	41	AC011553 Homo sapi
18	53	0.6	98261	10	HS105424 Homo sapi
19	52	0.6	123585	11	AC004707 Homo sapi
20	51	0.6	100267	40	HS88517 Homo sapi
21	51	0.6	129811	32	HS167219 Homo sapi
22	51	0.6	130082	32	HS167219 Homo sapi
23	51	0.6	144387	32	HS167219 Homo sapi
24	51	0.6	183285	42	AC009833 Homo sapi
25	50	0.6	132418	33	AC006357 Homo sapi
26	50	0.6	164905	42	AC007097 Homo sapi
27	50	0.6	187278	44	AC010192 Homo sapi
28	49	0.5	154347	43	AC013612 Homo sapi
29	49	0.5	168385	44	AC016032 Homo sapi
30	49	0.5	186711	43	AC011857 Homo sapi
31	49	0.5	205439	41	AC011400 Homo sapi
32	49	0.5	264977	42	AC009061 Homo sapi
33	48	0.5	483	9	HS88517 Homo sapi
34	48	0.5	56078	32	HS167219 Homo sapi
35	48	0.5	86408	33	AC007952 Homo sapi
36	48	0.5	98240	40	AC006021 Homo sapi
37	48	0.5	119694	32	HS167219 Homo sapi
38	48	0.5	172048	10	HS179N16 Homo sapi
39	48	0.5	177540	40	AC006538 Homo sapi
40	48	0.5	179865	41	AC007375 Homo sapi
41	48	0.5	184939	44	AC013682 Homo sapi
42	48	0.5	194612	41	AC008569 Homo sapi
43	48	0.5	256694	41	AC009280 Homo sapi
44	48	0.5	298966	32	HS167219 Homo sapi
45	47	0.5	101215	40	AC006966 Homo sapi

ALIGNMENTS

RESULT 1
AF123653
LOCUS AF123653 9108 bp DNA
DEFINITION Homo sapiens FEZ1 (FEZ1) gene, complete cds.
ACCESSION AF123653
VERSION AF123653.1 GI:4572463

07-APR-1999

10

RESULT 43056 DNA 172 bp STS 27-JAN-1999
LOCUS WTAFL1517-STS Human THUDSON SANGER Homo sapiens STS genomic,
DEFINITION sequence tagged site.
G43056
G43056.1 GI:4191973
STS.
Homo sapiens
SOURCE
ORGANISM
REFERENCE
AUTHORS
Wang,D.G., Fan,J.B., Siao,C.J., Berno,A., Young,P., Sapolsky,R.,
Ghandour,G., Perkins,N., Winchester,E., Spencer,J., Kruglyak,L.,
Stein,L., Hale,L., Topaloglou,T., Hubbell,E., Robinson,E.,
Mittmann,M., Morris,M.S., Shen,N., Kilburn,D., Rioux,J.,
Nusbaum,C., Rozen,S., Hudson,T.J., Lipshutz,R., Chee,M. and
Lander,E.S.
TITLE Large-scale identification, mapping, and genotyping of
single-nucleotide polymorphisms in the human genome
JOURNAL Science 280 (5366), 1077-1082 (1998)
MEDLINE 98248615
COMMENT
Synonyms: stSG10118
Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu
Primer A: TAGGCTTACCTGGAACTAC
Primer B: CTCACGGGAGGAGAAAC
STS size: 172
PCR Profile:
Presoak: 94 degrees C for 4.00 minutes
Denaturation: 94 degrees C for 50.0 seconds
Annealing: 58 degrees C for 1.50 minutes
Polymerization: 72 degrees C for 1.00 minutes
PCR Cycles: 30
Thermal Cycler: custom built by IAS, Costar, Cambridge MA

Protocol:
Template: 10 ng
Primer: each 5 pM
dNTPs: 4 mM
Taq Polymerase: 0.5 U
Total Vol: 20 uL

Buffer:
Mg2+: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
Gelatin: .001 %.
Location/Qualifiers
1. .172
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="42.70 cr from top of Chr8 linkage group"
/clone_lib="Human Thudson SANGER"
/note="human STS created from EST in the Sanger database"

STS
primer_bind 1. .172
primer_bind 1. .172
BASE COUNT 36 a 58 c 34 g 43 t 1 others
ORIGIN

Query Match 1.38; Score 121; DB 13; Length 172;
Best Local Similarity 99.4%; Pred. No. 5.3e-56;
Matches 171; Conservative 0; Mismatches 1; Indels 0; Gaps

STS	/cvganism= homo sapiens"
primer_bind	67. .197
primer_bind	67. .88
BASE COUNT	complement(180. .197)
ORIGIN	85 a 48 c 43 g 65 t 9 others

<http://ftp.genome.washington.edu/RV/RepeatMasker.html>
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		gap of unknown length
1505	2265:	contig of 761 bp in length
		gap of unknown length
2266	3025:	contig of 760 bp in length
		gap of unknown length
3026	3791:	contig of 766 bp in length
		gap of unknown length
		contig of 817 bp in length
3792		gap of unknown length